Patent Claims

1. A method for the analysis of cytosine methylations, hereby characterized in that

a) the DNA to be investigated is reacted so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base-pairing behavior,

b) a promoter sequence is introduced into the DNA,

c) RNA is transcribed,

d) the RNA is analyzed,

e) a conclusion with regard to the methylation state of the DNA is made.

2. The method according to claim 1, further characterized in that in step b), the promoter sequence is ligated to the DNA.

3. The method according to one of claims 1-2, further characterized in that in step b), a PCR is carried out, in which one of the primers bears a promoter sequence.

4. The method according to one of claims 1-2, further characterized in that in step b), an NASBA or another amplification method based on transcription is utilized.

5. The method according to one of claims 1-4, further characterized in that T3, T7 or SP6 promoters are used as promoters.

6. The method according to one of claims 1-5, further characterized in that the analysis of the RNA in step d) is conducted by means of a hybridization on an oligomer array.

7. The method according to one of claims 1-5, further characterized in that the analysis of the RNA in step d) is performed in a mass spectrometer.

8. A method for the analysis of cytosine methylations in DNA, characterized in that the following steps are conducted:

a) the DNA to be investigated is reacted so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base-pairing behavior,

b) the converted DNA is amplified by means of an amplification method based on transcription,

c) the amplificates are analyzed,

d) the methylation state of the investigated DNA is concluded.

9. A method for the analysis of cytosine methylations in DNA, characterized in that the following steps are conducted:

a) the DNA to be investigated is reacted so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base-pairing behavior,

b) the converted DNA is amplified by means of an amplification method based on transcription, wherein the amplification occurs in the presence of at least one methylation-specific blocker molecule, which binds specifically to the background nucleic acid and hinders the amplification thereof,

c) the amplificates are analyzed,

d) the methylation state of the investigated DNA is concluded.

10. The method according to claim 9, further characterized in that the blocker molecules form DNA-RNA hybrids with the background RNA, the RNA part of which is decomposed in the course of the amplification cycle.

11. The method according to one of claims 9-10, further characterized in that the blocker involves an oligonucleotide which bears at least one methylation-specific dinucleotide.

12. The method according to one of claims 8-11, further characterized in that the amplificates are detected by means of real-time probes.

13. The method according to one of claims 1-7, further characterized in that the RNA is chemically or enzymatically fragmented prior to the analysis in step d).

14. The method according to claim 13, further characterized in that the fragmenting is conducted as a function of the methylation pattern of the investigated DNA.

15. The method according to claim 14, further characterized in that the fragmenting is conducted by means of the enzyme RNase-T1.

16. The method according to one of claims 14-15, further characterized in that the analysis of the fragments is conducted by means of MALDI-TOF, by means of electrophoretic methods or by means of chromatographic methods.

17. The method according to one of claims 14-16, further characterized in that, in addition to the promoter, control sequences are additionally introduced into the DNA, and these form the basis for being able to examine whether the fragmenting is complete.

18. Use of the method according to claims 1-17 for the diagnosis or prognosis of cancer disorders or other diseases associated with a modification of the cytosine methylation state, for predicting undesired drug effects, for establishing a specific drug therapy, for monitoring the result of a drug therapy, for distinguishing cell types or tissues and for investigating cell differentiation.

19. A kit, which consists of a bisulfite reagent and of at least one primer which bears a promoter sequence.

20. A kit according to claim 19, which additionally contains enzymes and/or other components for conducting an amplification method based on transcription.

21. A kit according to claim 20, which additionally contains at least one methylation-specific blocker oligomer.

22. A kit, which consists of a bisulfite reagent, primers and an enzyme which cleaves RNA in a nucleotide-specific manner, and, optionally, a polymerase and other reagents necessary for an amplification.